

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: November 17, 2005, 23:58:38 ; Search time 42 Seconds

(without alignments)
579.419 Million cell updates/sec

Title: SEQ2-129X-307X

Perfect score: 1743

Sequence: 1 ASKKGVSFPLACSRSTSE.....XHEALHHYTKSLSLSPSK 326

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*

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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	100.0	326	2	US-08-656-586-9
2	1731	99.3	451	4	US-09-472-087-70
3	1731	99.3	463	4	US-09-472-087-1
4	1731	99.3	463	4	US-09-472-087-4
5	1731	99.3	463	4	US-09-472-087-63
6	1731	99.3	463	4	US-09-472-087-68
7	1731	99.3	464	4	US-09-472-087-2
8	1731	99.3	464	4	US-09-472-087-66
9	1731	99.3	470	4	US-09-859-053-28
10	1731	99.3	470	4	US-09-859-053-32
11	1731	99.3	470	4	US-09-859-053-36
12	1731	99.3	530	3	US-08-477-4608-4
13	1731	99.3	530	3	US-08-379-516-4
14	1731	99.3	530	3	US-09-329-916-4
15	1731	99.3	530	3	US-08-485-372A-4
16	1731	99.3	530	3	US-09-409-006A-4
17	1731	99.3	530	4	US-08-484-681-4
18	1731	99.3	530	4	US-09-766-995-4
19	1731	99.3	530	5	PCT-US93-07422-4
20	1728.5	99.2	462	4	US-09-627-896B-24
21	1725	99.0	463	4	US-09-472-087-64
22	1720	98.7	450	2	US-08-788-800-12
23	1720	98.7	469	2	US-07-934-373C-23
24	1720	98.7	469	3	US-08-437-642B-23
25	1720	98.7	469	4	US-08-146-206C-23
26	1720	98.7	469	4	US-09-705-686-23
27	1720	98.7	469	4	US-09-705-392A-23

28	1720	98.7	469	4	US-09-705-398-23	Sequence 23, Appl
29	1695	96.7	552	5	PCT-US93-07832-23	Sequence 23, Appl
30	1591.5	91.3	467	3	US-08-523-894-12	Sequence 12, Appl
31	1588	91.1	330	4	US-09-301-593-22	Sequence 22, Appl
32	1588	91.1	450	4	US-09-996-288-208	Sequence 208, App
33	1588	91.1	450	4	US-09-996-288-210	Sequence 210, App
34	1588	91.1	450	4	US-09-996-288-212	Sequence 212, App
35	1588	91.1	450	4	US-09-996-288-214	Sequence 214, App
36	1588	91.1	450	4	US-09-996-288-216	Sequence 216, App
37	1588	91.1	450	4	US-09-996-288-218	Sequence 218, App
38	1588	91.1	450	4	US-09-996-288-220	Sequence 220, App
39	1588	91.1	450	4	US-09-996-288-222	Sequence 222, App
40	1588	91.1	450	4	US-09-996-288-224	Sequence 224, App
41	1588	91.1	450	4	US-09-996-288-226	Sequence 226, App
42	1588	91.1	450	4	US-09-996-288-228	Sequence 228, App
43	1588	91.1	450	4	US-09-996-288-232	Sequence 232, App
44	1588	91.1	450	4	US-09-996-288-234	Sequence 234, App
45	1588	91.1	450	4	US-09-996-288-236	Sequence 236, App

ALIGNMENTS

RESULT 1
US-08-656-586-9
; Sequence 9, Application US/08656586
; Patent No. 5834597
; GENERAL INFORMATION:
; APPLICANT: Tso, J. Yun
; APPLICANT: Cole, Michael S.
; APPLICANT: Anasetti, Claudio
; TITLE OF INVENTION: Mutated No. 5834597activating Igg2 Domains and
; TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,586
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-007210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..326
; OTHER INFORMATION: /note= "heavy chain constant region of
; OTHER INFORMATION: Igg2 mutant 3"
US-08-656-586-9
Query Match 100.0%; Score 1743; DB 2; Length 326;
Best Local Similarity .99.4%; Pred. NO. 3.4e-153;

Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
Db 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
Qy 61 GLYSLSSVTVTPSSNFGTQTYTCNVDPKPSNTKVDKTKVERKCCVCEPCPCAPPAAAPSVF 120
Db 61 GLYSLSSVTVTPSSNFGTQTYTCNVDPKPSNTKVDKTKVERKCCVCEPCPCAPPAAAPSVF 120
Qy 121 LFPKPKDXLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
Db 121 LFPKPKDXLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
Qy 181 VVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYITLPPSREEMTKN 240
Db 181 VVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYITLPPSREEMTKN 240
Qy 241 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPMLDSGDSFPLYSKLTVDKSRWQQGN 300
Db 241 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPMLDSGDSFPLYSKLTVDKSRWQQGN 300
Qy 301 VFSCSVHAEALHNHYTQKSLSLSPSK 326
Db 301 VFSCSVHAEALHNHYTQKSLSLSPSK 326

RESULT 2

US-09-472-087-70
; Sequence 70, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, EILLEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: ABX-PF1

; CURRENT APPLICATION NUMBER: US/09/472,087

; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/113,647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 70

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-472-087-70

Query Match 99.3%; Score 1731; DB 4; Length 451;

Best Local Similarity 98.5%; Pred. No. 7.1e-152;

Matches 321; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 126 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 185
Qy 61 GLYSLSSVTVTPSSNFGTQTYTCNVDPKPSNTKVDKTKVERKCCVCEPCPCAPPAAAPSVF 120
Db 186 GLYSLSSVTVTPSSNFGTQTYTCNVDPKPSNTKVDKTKVERKCCVCEPCPCAPPAAAPSVF 245
Qy 121 LFPKPKDXLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
Db 246 LFPKPKDXLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 305
Qy 181 VVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYITLPPSREEMTKN 240
Db 306 VVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYITLPPSREEMTKN 365

Qy 241 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPMLDSGDSFPLYSKLTVDKSRWQQGN 300
Db 366 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPMLDSGDSFPLYSKLTVDKSRWQQGN 425
Qy 301 VFSCSVHAEALHNHYTQKSLSLSPSK 326
Db 426 VFSCSVHAEALHNHYTQKSLSLSPSK 451

RESULT 3

US-09-472-087-1

; Sequence 1, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, EILLEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: ABX-PF1

; CURRENT APPLICATION NUMBER: US/09/472,087

; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/113,647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 463

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-472-087-1

Query Match 99.3%; Score 1731; DB 4; Length 463;

Best Local Similarity 98.5%; Pred. No. 7.4e-152;

Matches 321; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 138 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 197
Qy 61 GLYSLSSVTVTPSSNFGTQTYTCNVDPKPSNTKVDKTKVERKCCVCEPCPCAPPAAAPSVF 120
Db 198 GLYSLSSVTVTPSSNFGTQTYTCNVDPKPSNTKVDKTKVERKCCVCEPCPCAPPAAAPSVF 257
Qy 121 LFPKPKDXLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
Db 258 LFPKPKDXLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 317
Qy 181 VVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYITLPPSREEMTKN 240
Db 318 VVSVLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYITLPPSREEMTKN 377
Qy 241 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPMLDSGDSFPLYSKLTVDKSRWQQGN 300
Db 378 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPMLDSGDSFPLYSKLTVDKSRWQQGN 437
Qy 301 VFSCSVHAEALHNHYTQKSLSLSPSK 326
Db 438 VFSCSVHAEALHNHYTQKSLSLSPSK 463

RESULT 4

US-09-472-087-4

; Sequence 4, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, EILLEN E.

; APPLICANT: HANKE, JEFFREY H.

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protein - protein search, using sw model

on: November 17, 2005, 23:47:57 ; Search time 164 Seconds
(without alignments)
768.804 Million cell updates/sec

File: SEQ2-129X-307X
Effect score: 1743
Sequence: 1 ASTKGPSVPLAPCSRSTSE.....XHEALHNYTQKLSLSPSK 326

oring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

arched: 2105692 seqs, 386760381 residues

tal number of hits satisfying chosen parameters: 2105692

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

slut No.	Score	Query Match %	Length	DB ID	Description
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2	1738	99.7	326	2	Aaw36163 Heavy cha
3	1731	99.3	326	4	Aae02643 Human imm
4	1731	99.3	326	5	Aam47857 Human Ig-
5	1731	99.3	326	5	Abg30462 Human ant
6	1731	99.3	326	5	Abg77148 Anti-IGF-
7	1731	99.3	326	6	Aae32916 Human imm
8	1731	99.3	326	6	Aae32628 Human imm
9	1731	99.3	326	6	Aao30894 Human imm
10	1731	99.3	326	7	Adf75002 Human Igg
11	1731	99.3	326	7	Adf75002 Human Ig
12	1731	99.3	326	8	Adm41541 Anti-inte
13	1731	99.3	326	8	Adq95469 Human Igg
14	1731	99.3	326	8	Adr28562 Human ant
15	1731	99.3	326	2	Aay31670 Human Igg
16	1731	99.3	445	8	Adk52332 Human ant
17	1731	99.3	445	8	Adk52384 Human ant
18	1731	99.3	445	8	Adk52296 Human ant
19	1731	99.3	445	8	Adk52312 Human ant
20	1731	99.3	451	3	Aay93734 The heavy
21	1731	99.3	451	6	Aae35889 Human 11.
22	1731	99.3	458	8	Adp07903 Human imm
23	1731	99.3	462	3	Aab26884 Human imm
24	1731	99.3	463	3	Aay93701 The heavy
25	1731	99.3	463	3	Aay93727 The heavy

26	1731	99.3	463	3	Aay93707 The heavy
27	1731	99.3	463	3	Aay93732 The heavy
28	1731	99.3	463	6	Aae35882 Human 4.1
29	1731	99.3	463	6	Aae35887 Human 6.1
30	1731	99.3	463	8	Adm41569 Anti-inte
31	1731	99.3	464	3	Aay93730 The heavy
32	1731	99.3	464	3	Aay93703 The heavy
33	1731	99.3	464	6	Aae35885 Human 4.8
34	1731	99.3	464	7	Ade28411 Human ant
35	1731	99.3	465	7	Ade28459 Human ant
36	1731	99.3	465	8	Adm41557 Anti-inte
37	1731	99.3	465	8	Adm41563 Anti-inte
38	1731	99.3	466	7	Adm28471 Human ant
39	1731	99.3	466	7	Adm28419 Human ant
40	1731	99.3	466	7	Adm28479 Human ant
41	1731	99.3	467	6	Abp71365 Anti-OPGL
42	1731	99.3	469	7	Ade28463 Human ant
43	1731	99.3	470	5	Aau74298 Anti-huma
44	1731	99.3	470	5	Aau74300 Anti-huma
45	1731	99.3	470	5	Aau74296 Anti-huma

ALIGNMENTS

RESULT 1
ADN33229
ID ADN33229 standard; protein; 326 AA.

XX AC ADN33229;
XX DT 18-NOV-2004 (first entry)
XX DE IGG2M3-CH heavy chain constant region.
XX IGG2M3-CH; antibody; IGG; heavy chain constant region;
KW FcRn binding affinity; asthma; autoimmune disease; cancer;
KW viral infection; antiasthmatic; immunosuppressive; cytostatic; virucide.
XX OS Unidentified.

XX PN WO2004035752-A2.

XX PD 29-APR-2004.

XX PF 15-OCT-2003; 2003WO-US033037.

XX PR 15-OCT-2002; 2002US-0418972P.

XX PR 10-APR-2003; 2003US-0462014P.

XX PR 03-JUN-2003; 2003US-0475762P.

XX PA 29-AUG-2003; 2003US-0499048P.

XX PI (PROT-) PROTEIN DESIGN LABS INC.

XX PI Hinton PR, Teurushita N, Tso YJ, Vasquez M;

XX WPI; 2004-348446/32.

XX PT New modified antibody of class IGG having an altered FcRn binding

XX PT affinity and/or serum half-life, useful in immunology and protein

XX PT engineering, and for diagnosing or treating asthma, autoimmune diseases,

XX PT cancer and viral infections.

XX PS Disclosure; SEQ ID NO 2; 140pp; English.

XX CC The invention relates to a modified antibody of class IGG where at least

XX CC one amino acid residue from the heavy chain constant region is different

XX CC from that present in an unmodified class IGG antibody, and where the FcRn

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protein - protein search, using sw model

on: November 18, 2005, 00:07:19 ; Search time 164 Seconds
(without alignments)
831.716 Million cell updates/sec

le: SEQ2-129X-307X
fect score: 1743
uence: 1 ASTKGSVFPPLACSRSTSE.....XHEALHNHYTKSLSPSK 326

ring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

ched: 1867879 seqs, 418409474 residues

al number of hits satisfying chosen parameters: 1867879

imum DB seq length: 0
imum DB seq length: 2000000000

it-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

.abase : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pap.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pap.*
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19: /cgn2_6/ptodata/1/pubaa/US11A_PUBCOMB.pap.*
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21: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pap.*
22: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1743	100.0	326	17	US-10-822-300-2
2	1743	100.0	326	17	US-10-822-300-10
3	1743	100.0	326	17	US-10-822-300-11
4	1743	100.0	326	17	US-10-822-300-12
5	1743	100.0	326	17	US-10-822-300-13
6	1743	100.0	326	17	US-10-822-300-14
7	1743	100.0	326	17	US-10-822-300-15
8	1743	100.0	326	17	US-10-822-300-16
9	1743	100.0	326	17	US-10-822-300-17
10	1743	100.0	326	17	US-10-822-300-18
11	1743	100.0	326	17	US-10-822-300-19

12	1743	100.0	326	17	US-10-822-300-20	Sequence 20, Appl
13	1743	100.0	326	17	US-10-822-300-21	Sequence 21, Appl
14	1743	100.0	326	17	US-10-822-300-22	Sequence 22, Appl
15	1743	100.0	326	17	US-10-822-300-23	Sequence 23, Appl
16	1743	100.0	326	17	US-10-822-300-24	Sequence 24, Appl
17	1743	100.0	326	17	US-10-822-300-25	Sequence 25, Appl
18	1743	100.0	326	17	US-10-822-300-26	Sequence 26, Appl
19	1743	100.0	326	17	US-10-822-300-27	Sequence 27, Appl
20	1743	100.0	326	17	US-10-822-300-28	Sequence 28, Appl
21	1743	100.0	326	17	US-10-822-300-48	Sequence 48, Appl
22	1743	100.0	326	17	US-10-822-300-49	Sequence 49, Appl
23	1743	100.0	326	17	US-10-822-300-50	Sequence 50, Appl
24	1743	100.0	326	17	US-10-822-300-51	Sequence 51, Appl
25	1743	100.0	326	17	US-10-822-300-52	Sequence 52, Appl
26	1743	100.0	326	17	US-10-822-300-53	Sequence 53, Appl
27	1743	100.0	326	17	US-10-822-300-54	Sequence 54, Appl
28	1743	100.0	326	17	US-10-822-300-55	Sequence 55, Appl
29	1743	100.0	326	17	US-10-822-300-56	Sequence 56, Appl
30	1743	100.0	326	17	US-10-822-300-57	Sequence 57, Appl
31	1743	100.0	326	17	US-10-822-300-58	Sequence 58, Appl
32	1743	100.0	326	17	US-10-822-300-59	Sequence 59, Appl
33	1743	100.0	326	17	US-10-822-300-60	Sequence 60, Appl
34	1743	100.0	326	17	US-10-822-300-61	Sequence 61, Appl
35	1743	100.0	326	17	US-10-822-300-62	Sequence 62, Appl
36	1743	100.0	326	17	US-10-822-300-63	Sequence 63, Appl
37	1743	100.0	326	17	US-10-822-300-64	Sequence 64, Appl
38	1743	100.0	326	17	US-10-822-300-65	Sequence 65, Appl
39	1743	100.0	326	17	US-10-822-300-66	Sequence 66, Appl
40	1743	100.0	326	17	US-10-822-300-72	Sequence 72, Appl
41	1743	100.0	326	17	US-10-822-300-73	Sequence 73, Appl
42	1743	100.0	326	17	US-10-822-300-74	Sequence 74, Appl
43	1743	100.0	326	17	US-10-687-118-2	Sequence 2, Appl
44	1743	100.0	326	17	US-10-687-118-10	Sequence 10, Appl
45	1743	100.0	326	17	US-10-687-118-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-822-300-2
; Sequence 2, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822.300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-822-300-2

Query Match 100.0%; Score 1743; DB 17; Length 326;
Best Local Similarity 99.4%; Pred. No. 6.7e-127;
Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	ASTKGSVFPPLACSRSTSESTAALGLVKDYFPPEPTVSNWNSGALTSGVHTFPAVLSS 60
DB	1	ASTKGSVFPPLACSRSTSESTAALGLVKDYFPPEPTVSNWNSGALTSGVHTFPAVLSS 60
QY	61	GLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKYDKTVVERKCCVCEPCPPAAPAAPSVF 120
DB	61	GLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKYDKTVVERKCCVCEPCPPAAPAAPSVF 120
QY	121	LFPPKPKDXLMSITPEVTCTVVVDVSHEDPPVQVNWYDGVGVHNAKTKPREEQNFSTR 180
DB	121	LFPPKPKDXLMSITPEVTCTVVVDVSHEDPPVQVNWYDGVGVHNAKTKPREEQNFSTR 180

181 VSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
|||||
181 VSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
|||||
241 QVSLTCLVKGYFSPYSDIAVEFESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQOQN 300
|||||
241 QVSLTCLVKGYFSPYSDIAVEFESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQOQN 300
|||||
301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
|||||
301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
|||||

ULT 2
10-822-300-10
sequence 10, Application US/10822300
Publication No. US20050014934A1
GENERAL INFORMATION:
APPLICANT: Hinton, et al.
TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.CPUS01
CURRENT APPLICATION NUMBER: US/10/822,300
CURRENT FILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
10-822-300-10

Query Match 100.0%; Score 1743; DB 17; Length 326;
Best Local Similarity 99.4%; Pred. No. 6.7e-127;
Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 60
|||||
1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 60
|||||
61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKTVKCKCCVECPCCPAPPAAPSVP 120
|||||
61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKTVKCKCCVECPCCPAPPAAPSVP 120
|||||
121 LFPPKPKDLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQFNSTFR 180
|||||
121 LFPPKPKDLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQFNSTFR 180
|||||
181 VSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
|||||
181 VSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
|||||
241 QVSLTCLVKGYFSPYSDIAVEFESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQOQN 300
|||||
241 QVSLTCLVKGYFSPYSDIAVEFESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQOQN 300
|||||
301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
|||||
301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
|||||

ULT 3
10-822-300-11
sequence 11, Application US/10822300
Publication No. US20050014934A1
GENERAL INFORMATION:
APPLICANT: Hinton, et al.
TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.CPUS01
CURRENT APPLICATION NUMBER: US/10/822,300
CURRENT FILING DATE: 2004-04-09

NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
US-10-822-300-11

Query Match 100.0%; Score 1743; DB 17; Length 326;
Best Local Similarity 99.4%; Pred. No. 6.7e-127;
Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 60
DB 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 60
QY 61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKTVKCKCCVECPCCPAPPAAPSVP 120
DB 61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKTVKCKCCVECPCCPAPPAAPSVP 120
QY 121 LFPPKPKDLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQFNSTFR 180
DB 121 LFPPKPKDLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQFNSTFR 180
QY 181 VSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
DB 181 VSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
QY 241 QVSLTCLVKGYFSPYSDIAVEFESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQOQN 300
DB 241 QVSLTCLVKGYFSPYSDIAVEFESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQOQN 300
QY 301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
DB 301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
|||||

RESULT 4
US-10-822-300-12
Sequence 12, Application US/10822300
Publication No. US20050014934A1
GENERAL INFORMATION:
APPLICANT: Hinton, et al.
TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.CPUS01
CURRENT APPLICATION NUMBER: US/10/822,300
CURRENT FILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
US-10-822-300-12

Query Match 100.0%; Score 1743; DB 17; Length 326;
Best Local Similarity 99.4%; Pred. No. 6.7e-127;
Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 60
DB 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 60
QY 61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKTVKCKCCVECPCCPAPPAAPSVP 120
DB 61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKTVKCKCCVECPCCPAPPAAPSVP 120
QY 121 LFPPKPKDLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQFNSTFR 180
DB 121 LFPPKPKDLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQFNSTFR 180
QY 181 VSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240

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protein - protein search, using sw model

on: November 17, 2005, 23:56:58 ; Search time 40 Seconds
(without alignments)
784.167 Million cell updates/sec

le: SEQ2-129X-307X

fect score: 1743

uence: 1 ASTKGPVSFPLAPCSRSTSE.....XHEALHNHYTKSLSLSPSK 326

ring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

ched: 283416 seqs, 96216763 residues

al number of hits satisfying chosen parameters: 283416

imum DB seq length: 0

imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Query	Score	Match	Length	DB	ID	Description
1	1731	99.3	326	1	G2HU		Ig gamma-2 chain C
2	1583.5	90.8	327	1	G4HU		Ig gamma-4 chain C
3	1582	90.8	330	1	GHU		Ig gamma-1 chain C
4	1558.5	89.4	377	2	A23511		Ig gamma-3 chain C
5	1549.5	88.9	377	2	A60764		Ig gamma-3 chain C
6	1254	71.9	328	2	I47159		Ig gamma 2a chain
7	1248	71.6	328	2	I47160		Ig gamma 2b chain
8	1222	70.1	328	2	I47161		Ig gamma 3 chain c
9	1212	69.5	328	2	I47158		Ig gamma 1 chain c
10	1185.5	68.0	472	2	S31459		Ig gamma-1 chain c
11	1178.5	67.6	472	2	S31459		Ig gamma-1 chain c
12	1164	66.8	326	2	PS0017		Ig heavy chain pre
13	1162.5	66.7	470	2	S22080		Ig heavy chain pre
14	1156	66.3	444	2	PC4436		monoclonal antibod
15	1150.5	66.0	329	1	G2GP		Ig gamma-2 chain C
16	1140	65.4	324	1	G1NS		Ig gamma-1 chain C
17	1135	65.1	393	1	G1NSM		Ig gamma-1 chain C
18	1134.5	65.1	374	2	S69339		Ig gamma-1 chain C
19	1129	64.8	255	4	S31866		Ig heavy chain V r
20	1126.5	64.6	308	2	C30554		Ig gamma-1 chain C
21	1120	64.3	322	2	PS0109		Ig gamma-2a chain
22	1118	64.1	334	2	PT0207		Ig gamma chain C r
23	1108.5	63.6	333	2	PS0018		Ig gamma-2b chain
24	1107.5	63.5	329	2	S00847		Ig gamma-2c chain
25	1100.5	63.1	327	2	S06611		Ig gamma-2 chain C
26	1096	62.9	289	1	G3HUW1		Ig gamma-3 heavy c
27	1085	62.2	329	1	G3MWC		Ig gamma-3 chain C
28	1082	62.1	330	1	G2NSA		Ig gamma-2a chain
29	1082	62.1	469	2	S37483		Ig gamma-2a chain

30	1080	62.0	398	1	G3MSM		Ig gamma-3 chain C
31	1077.5	61.8	335	1	G2MSAB		Ig gamma-2a chain
32	1077	61.8	339	1	G2MSAB		Ig gamma-2a chain
33	1067	61.2	446	2	S40295		Ig gamma-2a chain
34	1051	60.3	277	2	I47162		Ig gamma 4 chain c
35	1043	59.8	405	1	G2MSBM		Ig gamma-2b chain
36	1026	58.9	475	2	S01321		Ig gamma-2b chain
37	1025.5	58.8	474	1	G2MS11		Ig gamma heavy cha
38	695	39.9	180	2	I46732		Ig epsilon chain C
39	673.5	38.6	548	2	S38864		Ig heavy chain (DO
40	639	36.7	241	2	S69131		Ig gamma-1 chain C
41	574	32.9	152	2	S14236		Ig heavy chain VHI
42	567	32.5	249	2	S69340		Ig heavy chain pre
43	561	32.2	549	2	S04845		Ig heavy chain V-I
44	554	31.8	218	2	A36040		Ig heavy chain C r
45	519.5	29.8	448	2	S03186		Ig heavy chain C r

ALIGNMENTS

RESULT 1

G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L. U.S.A. 79, 1984-1988, 1982
Proc. Natl. Acad. Sci. U.S.A.
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; P1
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fi
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', '21-57', 'Z', '59', 'A', '61-193', 'D', '195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a l
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Z1e
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', '26-57', 'EV', '60-85', '132-171', 'ZZZ', '175', 'B', '177-193', 'D', '195-196', 'Q', '198-;
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Z1e
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Z1e, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds

rangione, B.; Milestein, C.; Pink, J.R.L.

ure 221, 145-148, 1969

itle: Structural studies of immunoglobulin G.

ference number: A93357; PMID:59064124; PMID:5782707

ontents: annotation; Sa, disulfide bonds

enetics:

ene: GDB:IGHG2

ross-references: GDB:119338; OMIM:147110

ap position: 1432.33-1432.33

omplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

n disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

uperfamily: immunoglobulin C region; immunoglobulin homology

eywords: duplication; glycoprotein; heterotetramer; immunoglobulin

0-85/Domain: immunoglobulin homology <IM1>

33-302/Domain: immunoglobulin homology <IM2>

39-306/Domain: immunoglobulin homology <IM3>

4/Disulfide bonds: interchain (to light chain) #status experimental

7-83,140-200,246-304/Disulfide bonds: #status experimental

02,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.3%; Score 1731; DB 1; Length 326;

est Local Similarity 98.5%; Pred. No. 1.2e-112;

atches 321; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKVERKCCVCCPCPPAPAAAPSVF 120

61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKVERKCCVCCPCPPAPVAGPSVF 120

121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

181 VSVSLTVVHODWLNKGEYKCKVSNKGLPAPIETKISITKQGPPEQVYTLPPSREEMTKN 240

181 VSVSLTVVHODWLNKGEYKCKVSNKGLPAPIETKISITKQGPPEQVYTLPPSREEMTKN 240

241 QVSLTCLVKGFPSPDIAVEVESNGQPENNYKTPPMLDSDGSGFFLYSKLTVDKSRWQQGN 300

241 QVSLTCLVKGFPSPDIAVEVESNGQPENNYKTPPMLDSDGSGFFLYSKLTVDKSRWQQGN 300

301 VFSCSVXHEALHNHYTKSLSPSK 326

301 VFSCSVXHEALHNHYTKSLSPGK 326

ULT 2

U

gamma-4 chain C region - human

pecies: Homo sapiens (man)

ate: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004

ccession: A90933; A90249; R02150

llison, J.; Buxbaum, J.; Hood, L.

1, 11-18, 1981

itle: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

ference number: A90933; PMID:83157104; PMID:6299662

ccession: A90933

olecule type: DNA

esidues: 1-327 <ELL>

ross-references: UNIPROT:P01861

ote: the sequence was determined from the germline gene

ink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

chem. J. 117, 33-47, 1970

itle: Human immunoglobulin subclones. Partial amino acid sequence of the constant

reference number: A90249; PMID:70207560; PMID:4192699

ccession: A90249

olecule type: protein

esidues: 1-30,81-326 <PIN>

enetics:

A;Gene: GDB:IGHG4

A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 1432.33-1432.33

A;Introns: 99/1; 111/1; 221/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>

F;99-110/Region: hinge

F;134-203/Domain: immunoglobulin homology <IM2>

F;240-307/Domain: immunoglobulin homology <IM3>

F;14/Disulfide bonds: interchain (to light chain) #status experimental

F;27-83,141-201,247-305/Disulfide bonds: #status predicted

F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.8%; Score 1593.5; DB 1; Length 327;

Best Local Similarity 91.1%; Pred. No. 2e-102;

Matches 298; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

QY 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKVERKCCVCCPCPPAPP-AAAPSV 119

Db 61 GLYSLSVVTVPSNFGTQTYTCNVDPKPSNTKVDKVERKCCVCCPCPPAPP-AAAPSV 120

QY 120 FLFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTF 179

Db 121 FLFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTF 180

QY 180 RVSVSLTVVHODWLNKGEYKCKVSNKGLPAPIETKISITKQGPPEQVYTLPPSREEMTK 239

Db 181 RVSVSLTVVHODWLNKGEYKCKVSNKGLPAPIETKISITKQGPPEQVYTLPPSREEMTK 240

QY 240 NOVSLTCLVKGFPSPDIAVEVESNGQPENNYKTPPMLDSDGSGFFLYSKLTVDKSRWQQG 299

Db 241 NOVSLTCLVKGFPSPDIAVEVESNGQPENNYKTPPMLDSDGSGFFLYSKLTVDKSRWQQG 300

QY 300 NVFSCSVXHEALHNHYTKSLSPSK 326

Db 301 NVFSCSVXHEALHNHYTKSLSLGK 327

RESULT 3

GHHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C;Accession: A93433; S33887; B90563; A90564; B91688; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; PMID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: UNIPROT:P01857; EMBL:217370

A;Note: this sequence has the Gim(17) allotypic marker, 97-Lys, and the Gim(1) markers, ;

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S38661

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:217370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a ;

A;Reference number: S33887; PMID:83001943; PMID:6811139

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protein - protein search, using sw model

on: November 17, 2005, 23:56:13 ; Search time 174 Seconds
(without alignments)
959.413 Million cell updates/sec

le: SEQ2-129X-307X

fect score: 1743

uence: 1 ASTKGPSVFLAPCSRSTSE.....XHEALHNHYTQKSLSLSPSK 326

ring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

ched: 1612378 seqs, 512079187 residues

al number of hits satisfying chosen parameters: 1612378

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB	ID	Description
1	1731	99.3	326	1	GC2_HUMAN	P01859 homo sapien
2	1731	99.3	417	2	Q6N093	Q6N093 homo sapien
3	1726	99.0	465	2	Q6P6C4	Q6P6C4 homo sapien
4	1717	98.5	493	2	Q68CN4	Q68CN4 homo sapien
5	1716	98.5	464	2	Q6MZU6	Q6MZU6 homo sapien
6	1588	91.1	348	2	Q6PYX1	Q6PYX1 homo sapien
7	1588	91.1	478	2	Q6PI81	Q6PI81 homo sapien
8	1588	91.1	480	2	Q6PJF1	Q6PJF1 homo sapien
9	1583.5	90.8	327	1	GC4_HUMAN	P01861 homo sapien
10	1583.5	90.8	473	2	Q8TC63	Q8TC63 homo sapien
11	1582	90.8	330	1	GC1_HUMAN	P01857 homo sapien
12	1582	90.8	465	2	Q6GMX6	Q6GMX6 homo sapien
13	1582	90.8	466	2	Q6IN78	Q6IN78 homo sapien
14	1582	90.8	469	2	Q6Z7P5	Q6Z7P5 homo sapien
15	1582	90.8	470	2	Q6PJ44	Q6PJ44 homo sapien
16	1582	90.8	470	2	Q7Z5W1	Q7Z5W1 homo sapien
17	1582	90.8	472	2	Q6N089	Q6N089 homo sapien
18	1582	90.8	475	2	Q6GMW7	Q6GMW7 homo sapien
19	1582	90.8	476	2	Q6GMX1	Q6GMX1 homo sapien
20	1580.5	90.7	476	2	Q6MZK7	Q6MZK7 homo sapien
21	1578	90.5	473	2	Q6MZV7	Q6MZV7 homo sapien
22	1578	90.5	473	2	Q6P055	Q6P055 homo sapien
23	1578	90.5	475	2	Q6MZQ6	Q6MZQ6 homo sapien
24	1578	90.5	480	2	Q6N094	Q6N094 homo sapien
25	1578	90.5	481	2	Q6N097	Q6N097 homo sapien
26	1578	90.5	482	2	Q7Z3S1	Q7Z3S1 homo sapien
27	1577	90.5	544	2	Q6PJ95	Q6PJ95 homo sapien
28	1575	90.4	466	2	Q6N096	Q6N096 homo sapien
29	1571	90.1	475	2	Q6N095	Q6N095 homo sapien
30	1561.5	89.6	521	2	Q6N4Y9	Q6N4Y9 homo sapien
31	1558.5	89.4	518	2	Q6N030	Q6N030 homo sapien

32	1556.5	89.3	509	2	Q8NFI7	Q8NFI7 homo sapien
33	1453.5	83.4	354	2	Q86TT2	Q86TT2 homo sapien
34	1193.5	68.5	337	2	Q95M34	Q95M34 equus caball
35	1185.5	68.0	323	1	GC_RABIT	P01870 oryctolagus
36	1164	66.8	326	1	GC1_RAT	P20759 rattus norv
37	1157	66.4	463	2	Q99LC4	Q99LC4 mus musculu
38	1156	66.3	458	2	Q652Q1	Q652Q1 homo sapien
39	1150.5	66.0	329	1	GC2_CAVPO	P01862 cavia porce
40	1140	65.4	324	1	GC1_MOUSE	P01868 mus musculu
41	1135	65.1	393	1	GC1W_MOUSE	P01869 mus musculu
42	1126	64.6	487	2	Q652L2	Q652L2 mus sp. fv/
43	1125	64.5	679	2	Q96P08	Q96P08 homo sapien
44	1120	64.3	322	1	GCA_RAT	P20760 rattus norv
45	1108.5	63.6	333	1	GCB_RAT	P20761 rattus norv

ALIGNMENTS

RESULT 1

ID	GC2_HUMAN	STANDARD;	PRT;	326 AA.
AC	P01859;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	19 gamma-2 chain C region.			
GN	Names=IGHG2;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RX	SEQUENCE OF 2-326 FROM N.A.			
RY	MEDLINE=82197621; PubMed=6804948;			
RA	Ellison J.W., Hood L.B.;			
RT	"Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant region genes";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).			
RN	[2]			
RP	SEQUENCE OF 88-115 FROM N.A.			
RC	TISSUE=Fetal liver;			
RX	MEDLINE=83001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;			
RA	Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;			
RT	"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";			
RN	Cell 29:671-679(1982).			
RN	[3]			
RP	SEQUENCE OF 99-177 AND 310-326 FROM N.A.			
RC	TISSUE=Fetal liver;			
RX	MEDLINE=84235982; PubMed=6329676;			
RA	Krawinkel U., Rabbitts T.H.;			
RT	"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";			
RL	EMBO J. 1:403-407(1982).			
RN	[4]			
RN	SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL);			
RP	MEDLINE=81007873; PubMed=6774012;			
RA	Wang A.-C., Tung E., Fudenberg H.H.;			
RT	"The primary structure of a human IgG2 Heavy chain: genetic, evolutionary, and functional implications.";			
RL	J. Immunol. 125:1048-1054(1980).			
RN	[5]			
RN	SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).			
RP	MEDLINE=80001357; PubMed=113060;			
RA	Connell G.E., Parr D.M., Hofmann T.;			
RT	"The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";			
RN	Can. J. Biochem. 57:758-767(1979).			
RN	[6]			
RP	SEQUENCE OF 238-275 (ZIE).			
RP	MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;			

Hofmann T., Parr D.M.;
 "A note of the amino acid sequence of residues 381-391 of human immunoglobulin gamma chains.";
 Mol. Immunol. 16:923-925(1979).
 [7]
 REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 Hofmann T., Parr D.M.;
 Submitted (MAR-1980) to the PIR data bank.
 [8]
 SEQUENCE OF 1-121 (DOT).
 MEDLINE=9525298; PubMed=7737190;
 Scoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 "Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";
 Eur. J. Biochem. 228:886-893(1995).
 [9]
 DISULFIDE BONDS.
 MEDLINE=72033500; PubMed=4940472;
 Milstein C., Frangione B.;
 "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 Biochem. J. 121:217-225(1971).
 [10]
 DISULFIDE BONDS.
 MEDLINE=69064124; PubMed=5782707;
 Frangione B., Milstein C., Pink J.R.L.;
 "Structural studies of immunoglobulin G.";
 Nature 221:145-148(1969).

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EMBL; J00230; AAB59393.1; --
 PIR; A93906; G2HU.
 HSP; P01857; 100X.
 Genew; HGNC:5526; IGHG2.
 MIN; 147110; --
 GO; GO:0005624; C:membrane fraction; NAS.
 GO; GO:0003823; F:antigen binding; NAS.
 GO; GO:0006955; P:immune response; NAS.
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003597; Ig_cl.
 InterPro; IPR003006; Ig_MHC.
 Pfam; PF00047; Ig; 3.
 SMART; SM00407; IGcl; 2.
 PROSITE; PS00835; IG_LIKE; 3.
 PROSITE; PS00290; IG_MHC; 2.

Direct protein sequencing; Immunoglobulin C region;

Immunoglobulin domain.

NON TER 1 1 CH1.
 DOMAIN 1 98 Hinge.
 DOMAIN 99 110 CH2.
 DOMAIN 111 219 CH2.
 DOMAIN 220 326 CH3.
 DISULFID 14 14 Interchain (with a light chain).
 DISULFID 27 83 Interchain (with a heavy chain).
 DISULFID 102 102 Interchain (with a heavy chain).
 DISULFID 103 103 Interchain (with a heavy chain).
 DISULFID 106 106 Interchain (with a heavy chain).
 DISULFID 109 109 Interchain (with a heavy chain).
 DISULFID 140 200
 DISULFID 246 304
 SITE 156 156
 VARIANT 60 60

At or near the complement-binding site.
 S -> A (in myeloma proteins TIL and ZIE).
 /FTid=VAR_003889.
 C -> S (in Ref. 3).

CONFLICT 109 109
 SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 99.3%; Score 1731; DB 1; Length 326;

Best Local Similarity 98.5%; Pred. No. 1.1e-116;
 Matches 321; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 QY 61 GLYSLSVVTVSPSSNFGTQYTCNVDPKPSNTKVDKTKVERKCCVCEPCPPAPPAAPSVF 120
 DB 61 GLYSLSVVTVSPSSNFGTQYTCNVDPKPSNTKVDKTKVERKCCVCEPCPPAPPAAPSVF 120
 QY 121 LPPPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVGVEVHNAAKTKPREQFNSTFR 180
 DB 121 LPPPKPKDLMISRTPEVTCVVVDVSHEDPEVQFNWYDGVGVEVHNAAKTKPREQFNSTFR 180
 QY 181 VVSVLTVVHODMLNGKEYCKVSNKGLPAPIETKTSTKGGQPREPOVYTLPPSREEMTKN 240
 DB 181 VVSVLTVVHODMLNGKEYCKVSNKGLPAPIETKTSTKGGQPREPOVYTLPPSREEMTKN 240
 QY 241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
 DB 241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
 QY 301 VFSCSVVHEALHNHYTQKSLSLSPSK 326
 DB 301 VFSCSVVHEALHNHYTQKSLSLSPSK 326

RESULT 2

Q6N093 PRELIMINARY; PRT; 417 AA.
 ID Q6N093
 AC Q6N093;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686I04196 (Fragment).
 GN Names=DKFZp686I04196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human CDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640623; CAE45777.1; --
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;

Query Match 99.3%; Score 1731; DB 2; Length 417;

Best Local Similarity 98.5%; Pred. No. 1.6e-116;
 Matches 321; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 DB 92 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 151